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SEQ ID NO: 6	A33	1	M	V	G	K	M	W	P	V	L	W	T	L	C	A	V	R	V	T	V	D	A	I	S	V	E	T	P	Q	D	V	L	R	A	S	O	G	K	S	V	T	L	P	C	T	Y	H	T	S				
SEQ ID NO: 1	40628	1	M	G	T	K	A	Q	V	E	R	K	L	C	L	F	I	L	A	I	L	C	S	L	A	L	G	S	V	T	V	H	S	E	P	E	V	R	I	P	E	
SEQ ID NO: 2	45416	1	M	G	I	L	L	G	L	L	L	G	H	L	T	V	D	T	Y	G	R	P	I	L	E	V	P	E	S	V	T	G	P	W	K	G	D	V	N	L	P	C	T	Y	O	P	L			
SEQ ID NO: 9	35638	1	M	A	R	R	S	R	H	R	L	L	L	L	R	Y	L	V	V	A	L	G	Y	H	K	A	Y	G	F	S	A	P	K	O	Q	V	T	A	V	E		
SEQ ID NO: 10	JAM	1	.	M	G	T	E	G	K	A	G	R	K	L	L	F	L	F	T	S	M	I	L	G	S	L	V	Q	G	K	S	V	Y	T	A	O	S	D	V	Q	V	P	E
A33		51	S	R	E	G	L	I	Q	W	D	K	L	L	L	T	H	T	E	R	V	I	W	P	F	S	N	K	N	Y	I	H	G	E	L	Y	K	N	R	V	S	I	S	N	A	E	Q	S	D	A				
40628		43	N	N	P	V	K	L	S	C	A	Y	S	G	F	S	S	P	R	V	E	W	K	F	D	Q	G	D	T	T	R	L	V	C	Y	N	N	K	I	T	A	S	Y	E	O	R	V	T	F	L	P	T		
45416		47	Q	G	Y	T	Q	V	L	V	K	W	L	V	Q	R	G	S	D	P	V	T	I	F	L	R	D	S	S	G	D	H	I	Q	A	K	Y	Q	G	R	L	H	V	S	H	K	V	P	G	D	V			
35638		43	Y	Q	E	A	I	L	A	C	K	T	P	K	T	V	S	S	R	L	E	W	K	L	G	R	S	V	S	F	V	Y	Q	T	L	Q	G	D	F	K	N	R	A	E	M	I	D	F						
JAM		42	N	E	S	I	K	L	T	C	T	Y	S	G	F	S	S	P	R	V	E	W	K	F	V	Q	G	S	T	T	A	L	V	C	Y	N	S	Q	I	T	A	P	Y	A	D	R	V	T	F	S	S			
A33		101	S	I	T	I	D	Q	L	T	M	A	D	N	G	T	Y	E	C	S	V	S	L	.	M
40628		93	G	I	T	F	K	S	V	T	R	E	D	T	G	T	Y	T	C	M	V	S	E	
45416		97	S	L	Q	L	S	T	L	E	M	D	D	R	S	H	Y	T	C	E	V	T	W	O	T	P	D	G	N	Q	V	V	R	D	K	I	T	E	L	R	V	Q	K	L	S	V	S	K	P	T	V	T		
35638		93	N	I	R	I	K	N	V	T	R	S	D	A	G	K	Y	R	C	E	V	S	A	P	S	
JAM		92	G	I	T	F	S	S	V	T	R	K	D	N	G	E	Y	T	C	M	V	S	E		
A33		144	P	E	C	G	I	E	G	E	T	I	G	N	I	O	L	T	C	Q	S	K	E	G	S	P	T	P	Q	Y	S	W	K	R	Y	N	I	L	N	Q	E	
40628		135	P	T	V	N	I	P	S	S	A	T	I	G	N	R	A	V	L	T	C	S	E	Q	D	G	S	P	P	S	E	Y	T	W	F	K	D	G	I	V	M	P	T	N	.	P	K	S	T	R	A	F		
45416		147	T	G	S	G	Y	G	F	T	V	P	Q	G	M	R	I	S	L	Q	C	Q	A	R	.	G	S	P	P	I	S	Y	I	W	Y	K	Q	O	T	N	N	Q	E	P		
35638		137	P	S	C	E	V	P	S	S	A	L	S	G	T	V	V	E	L	R	C	Q	D	K	E	G	N	P	A	P	E	Y	T	W	F	K	D	G	I	R	L	L	E	N	.	P	R	L	G	S	Q	S		
JAM		134	P	T	I	S	V	P	S	S	V	T	I	G	N	R	A	V	L	T	C	S	E	H	D	G	S	P	P	S	E	Y	S	W	F	K	D	G	I	S	M	L	T	A	D	A	K	K	T	R	A	F		

FIG.-1A

SEQ ID NO: 6 A33 186 ... PLAQPASGQPVS LKNI STDTSGYI CTSSNEEG... TQFCNITY
SEQ ID NO: 1 40628 184 SNSSYYLHPTTGE L VF DPL SAS DTGEYSCEARNGYG... TPMTSNAY
SEQ ID NO: 2 45416 188 ... IKVATLSTLLFKPAVIA DSGSYFCTAKGQV GSEQHSDIYKFVVKD
SEQ ID NO: 9 35638 186 TNSSYTMNTKTGT LQFN TV SKL DTGEYSCEARN SVG... YRRCPGKR
SEQ ID NO: 10 JAM 184 MNSSFTIDPKSGD L I F D P V T A F D S G E Y Y C O A Q N G Y G... TAMRSEAA

A33 227 AYRSPSMNVALYVGI AVGVVAA L I I I G I I Y C C C C R G K D D N T E D K E D A...
40628 228 RMEAVERNVGVIVAAVLVTL L L L G I L V F G I W F A Y S R G H F D R T K K G T S...
45416 233 SSKLLKTKTEAPT TMTYPLKATSTYKQSWD W T T D M D G Y L G E T S A G P G K S L
35638 230 WQVDDL N I S G I I A A V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S...
JAM 228 HMDAVELNVGGIVAAVLVTL L L L G L L I F G V W F A Y S R G Y F E T T K K G T A P...

A33 275 RPNREAYEEPPEQLREL SREREE EDDYRQEEQRSTGRES PDHLDQ
40628 275 ... SKKVIYSQPSARSEGEFKQTSSFLV...
45416 283 PVFAIILIIISLCCMVVFTWAYIMLCRKTSQOEHVVEAAR...
35638 277 NSSSKATTMSEN VQWLT PVI PAL WKAAAGGSRGQEF...
JAM 276 ... GKKV IYSQPSSTRSEGEFKQTSSFLV...

FIG. 1B

SEQ ID NO:1

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Lys Leu Leu Cys Lys Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr	1	5	10	15	20	25	30
Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val	35	40	45	50	55	60	
Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu	65	70	75	80	85	90	
Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Asn Ser Tyr Gly	95	100	105	110	115	120	
Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val	125	130	135	140	145	150	
Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr	155	160	165	170	175	180	
Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr	185	190	195	200	205	210	
Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val	215	220	225	230	235	240	
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys	245	250	255	260	265	270	
Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val	275	280	285	290	295	299	

FIG._2

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SEQ ID NO:2
 1 MCILLGLLL GHLTVDTYGR PILEVPESVT GPWKGDVNL P CTYDPLQCYT QVLVKKWLVR GSDPTIFLR DSSGDHIQQA KYQRLHVSH KVPGDVSLQL
 101 STLEMDDRSH YTCEVTWQTP DGNQVWRDKI TELRVQKLSV SKPTVTTCSG YGFTVPQGMH ISLQCCARGS PPISYIWKQ QTNQEPKIV ATLSTLLFXP
 ^Glycosaminoglycan attachment site
 201 AVIADSGSYF CTAKQGVSE QHSDIVKFV KDSSKLLKTK TEAPTTMTYP LKATSTVKQS WDWTMDMGY LGTSAGPGK SLPVFAIILI ISLCCMVVFT
 ^Transmembrane domain

FIG._3

301 MAYIMLCRKT SQEHVYEAA R

4 / 24

OLI2162 (35936.f1) SEQ ID NO:12 TCGCGGAGCTGTGTTCTGTTTCCC	OLI2166 (35936.f3) SEQ ID NO:16 TTGCCTTACTCAGGTGCTAC
OLI2163 (35936.p1) SEQ ID NO:13 TGATCGCGATGGGACAAAGGCGCAAGCTCGAGAGGAACTGTTGTGCCT	OLI2167 (35936.r2) SEQ ID NO:17 ACTCAGCAGTGGTAGGAAAG
OLI2164 (35936.f2) SEQ ID NO:14 ACACCTGGTTCAAAGATGGG	
OLI2165 (35936.r1) SEQ ID NO:15 TAGGAAGAGTTGCTGAAGGCACGG	

FIG._8

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DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100
GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
AACAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
TGTCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

FIG._4A

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
GCGCAAGCTC GAGAGGAAAC TGTGTGCCT CTTCATATTG GCGATCCTGT 150
TGTGCTCCCT GGCATTGGGC AGTGTTACAG TTGCACTCTT CTGAACCTGA 200
AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCTGTG GCCTACTCGG 250
GCTTTTCTTC TCCCCGTGTG GAGTGGAAGT TTGACCAAGG AGACACCACC 300
AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAGACA 400
CTGGGACATA CACTTGATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500
TAACATCCCC TCCTCTGCCA CCATTGGGAA CCGGGCAGTG CTGACATGCT 550
CAGAACAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTTGAT CCCCTGTCAG 700
CCTCTGATAC TGGAGAATAC AGCTGT 726

FIG._4B

consen02 SEQ ID NO:5

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
TAAGATTACT GAGCTCCGTG TCCAGAACT CTCTGTCTCC AAGCCCACAG 200
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT 400
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTG TG 650
CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAATA CTCTGATGAG 850
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
AGGGCAAAAG TGTCTGTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC 1000
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
CTCTCTTCCT GGATAGCCCA AAGTGTCGCG CTACCAACAC TGGAGCCGCT 1100
GGGAGTCACT GGCTTTGCCC TGGAATTTGC CAGATGCATC TCAAGTAAGC 1150
CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG 1300
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT 1400
TATTTACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
AAA 1503

FIG. 4C

SEQ ID NO:11 GGAGTCCTT CGCGGGCTGT TGTGTAGTG GCCTGATCGC GATGGGGACA AAGGGCGAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT 100
TGGCGATCCT GTTGTGCTCC CTGGCATTTG GCAGTGTTAC AGTGCACTCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AATCCTGTGA AGTTGTCCTG 200
TGCTACTCG GGCCTTTCTT CTCCCGGTGT GGAGTGAAG TTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCCTAT 300
GAGGACGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC ACGGGAAGAC ACTGGACAT ACACCTGTAT GGTCTCTGAG GAAGCGGCA 400
ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC CTCCTCTGCC ACCATTGGGA ACCGGGCAGT 500
GCTGACATGC TCAGAACAAG ATGGTTCCCC ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CCAAAAGCAC CCGTGCCCTC 600
AGCAACTCTT CCTATGTCCT GAATCCACCA ACAGGAGAGC TGCTCTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700
GGTATGGAC ACCCATGACT TCAAAATGCTG TCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800
GGGAATCTTG GTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA GAAAGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT 900
AGTGCCCGAA GTGAAGGAGA ATTCAAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCSCC TATCATCTGC AATTGCCCTTA CTCAGGTGCT 1000
ACCGGACTCT GGCCCTCTGAT GTCTGTAGTT TCACAGGATG CCTTATTGT CTTCTACACC CCACAGGGCC CCTACTTCT TCGGATGTGT TTTTAATAAT 1100
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAAT TGTTTAAAGT GTTTATTCCT CATTCTTTG 1200
AGGATCAGG AAGGAATCCT GGGATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGCGGGGGT TGCACCTCAC TGCCACCTG 1300
GCTGGCAGG ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGCTCTTT TGGTGTGAC TGACGACCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400
CTAGAGCGGC TGAATGGTT GTTTGGTGAT GACACTGGG TCCTTCCATC TCTGGGCCC ACTCTCTTCT GTCTTCCAT GGGAAAGTGCC ACTGGGATCC 1500
CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTGCTGT GGAATAATGG AGCTCTTGT GTGGAGAGCA TAGTAAATTT TCAGAGAACT 1600
TGAAGCCAAA AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAACTGGAG GCTGGGCGCA GTGGCTCAG CTGTAATCC CAGAGGCTGA GGCAGGCGGA 1700
TCACCTGAGG TCGGGAGTTC GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAAT ACAAGTTAG CCAGGCATGG TGGTGCAATG CTGTAGTCCC 1800
AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

FIG.-5

SEQ ID NO:7

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1  CCCACGGCTC GCGCCACGGG TCCGCCGCCA GCGCTCCGGG CCACAGNAG TTTCAGCCTC TTTGGTAGCA GGAGGCTGCA AGAAAGGACA
GGGTGGCGAG GCGGTGGCGC AGGCGGTGCC CCAGCGCGGT GCGAGGCCCC GGTGGTCTTC AACTCGGAG AAACCATCGT CCTCCGACCT TCTTTCCTGT

101 GAAGTAGCTC TGGCTGTGAT GGGGATCTTA CTGGGCTGCG TACTCTCTGG GCACCTAACA GTGGACACTT ATGCCCGTCC CATCCTGGAA GTGCCAGAGA
CTTCATCGAG ACCGACACTA CCCCTAGAAAT GACCCGGACG ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCGGCAGG GTAGGACCTT CACGGTCTCT

1      SEQ ID NO:2 M G I L L G L L L G L L G H L T V D T Y G R P I L E V P E S
^MET
201 GTGTAACAGG ACCTTGGAAA GGGGATCTGA ATCTTCCCTG CACCTATGAC CCCTGCGCAG GCTACACCCA AGTCTTGGTG AAGTGGCTGG TACAACGTGG
CACATTGTCC TGGAACTTTT CCCCTAGACT TAGAAGGGAC GTGGATACTG GGGACGTTT CCGATGTGGT TCAGAACCAC TTCACCGACC ATGTTGCACC
29 V T G P W K G D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCAGACCCT GTCACCATCT TTCTACGTGA CTCTTCTGGA GACCATATCC AGCAGGCAAA GTACCAGGGC GCGCTGCATG TCAGCCACAA GGTTCACAGA
GAGTCTGGGA CAGTGGTAGA AAGATGCACT GAGAACACCT CTGCTATAGG TCCTCCGTTT CATGGTCCCG GCGGACGTAC ACTCGGTGTT CCAAGGTCTT
62 S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G

401 GATGTATCCC TCCAATTGAG CACCCTGGAG ATGGATGACC GGAGCCACTA CACCTGTGAA GTCACTCTGC AGACTCCTGA TGGCAACCAA GTCGTGAGAG
CTACATAGGG AGGTAACTC GTGGGACCTC TACCTACTGG CCTCGTGTAT GTGCACACTT CAGTGGACCG TCTGAGGACT ACCGTTGTT CAGCACTCTC
95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATAAGATTAC TGAGCTCCGT GTCCAGAAAC TCTCTGTCTC CAAGCCACA GTGACAACTG GCACCGGTTA TGGCTTCACG GTGCCCCCAGG GAATGAGGAT
TATTCTAATG ACTCGAGGCA CAGGTCTTTG AGAGACAGAG GTTCGGGTGT CACTTTTGAC CGTCGCCAAT ACCGAAGTGC CACGGGTGCC CTTACTCCTA
129 K I T E L R V Q K L S V S K P T V T T G S G Y C F T V P Q G H R I

601 TAGCCTTCAA TGCCAGGCTC GGGGTTCTCC TCCCATCAGT TATATTGGT ATAAGCAACA GACTAATAAC CAGGAACCCA TCAAAGTAGC AACCCTAAGT
ATCGGAAGTT ACGGTCCGAG CCCCAGAGG AGGGTAGTCA ATATAAACCA TATTCTGTGT CTCATTATTG GTCCTTGGGT AGTTTCATCG TTGGGATTCA
162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

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FIG._6A

SEQ ID NO:7 701 ACCTTACTCT TCAAGCCTGC GGTGATAGCC GACTCAGGCT CCTATTCTTG CACTGCCAAG GGCCAGGTTG GCTCTGAGCA GCACAGGAC ATTGTGAAGT
TGGATCAGA AGTTCGGACG CCACTATCGG CTGAGTCCGA GGATAAGAC GTGACGGTTC CCGGTCCAC CGAGACTCGT CCGTTCGGTG TAACACTTCA

SEQ ID NO:2 195 T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F

801 TTGTGGTCAA AGACTCCTCA AAGCTACTCA AGACCAAGAC TGAGGCACCT ACAACCATGA CATACCCTT GAACAACA TCTACAGTGA AGCAGTCTTG
AACACCAGTT TCTGAGGAGT TTCGATGAGT TCTGGTCTG ACTCCGTGA TCTTGTACT GTATGGGAA CTTTCGTTGT AGATGTCAC TCGTCAGGAC

229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W

901 GGACTGGACC ACTGACATGG ATGGCTACCT TGGAGAGACC AGTGTGGC CAGGAAAGAG CCTGCTGTC TTGCCATCA TCCTCATCAT CTCCTTGTC
CCTGACCTGG TGACTGTACC TACCGATGGA ACCTCTCTGG TCACGACCG GTCTTTCTC GGACGACAG AACCGTAGT AGGAGTAGTA GAGGAACACG

262 D W T T D H D G Y L G E T S A G P G K S L P V F A I I L I I S L C

1001 TGTATGGTGG TTTTACCAT GGCCTATATC ATGCTCTGTC GGAGACATC CCAACAGAG CATGCTTACG AAGCAGCCAG GTAAGAAAGT CTCCTCTCTT
ACATACCACC AAAAATGGTA CCGGATATAG TACGAGACAG CTTCTGTAG GGTGTTCTC GTACAGATGC TTCTCGGTC CATCTTTCA GAGAGGAGAA

295 C H V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGA CCCCCTCCCT GGCCTCAATT TTGATTACTG GCAGGAATG TCGAGGAAG GGGTGTGGC ACACACCCAA TCCTAAGGCC GGAGCCCTTC
GGTAANAAT GGGCCAGGA CGGAGTTAA AACTAATGAC CGTCTTTAC ACCTCTTCC CCCCACACCG TGCTGGGTT AGGATTCCGG CTTCCGGAAG

1201 AGGTCAGGA CATAGCTGCC TTCCCTCTCT CAGGCACCT CTGAGTTCT TTTGGCCCTC TGAACACAA GGATAATTGA GATCCATCTG CCTTCTGCTT
TCCAGTCTCT GTATCGACGG AAGGAGAGA GTCCGTGGAA GACTCCAA GACTCCAACT ACTTGTTT CTTATTAAAT CTAGGTAGAC GGAAGACGAA

1301 CCAGAAATCC TGGGTGGTAG GATCCTGATA ATTAATTGCC AAGATTGAG GCAGAAAGGT GGGAAACAG GACCACAGCC CCAAGTCCCT TCTTATGGGT
GGTCTTAGG ACCCACCATC CTAGGACTAT TAATTAACCG TTCTTAATC CGTCTTCCA CCTTTGGTC CTGCTGTGG GGTTCAGGGA AGAATACCCA

1401 GGTGGGCTCT TGGGCCATAG GGCACATGCC ACAGAGGCCA ACCACTCTGG AGAACCATG AGGTGGCCA TCTTCCCAAG TGGCTGCTCC AGTATGAGC
CCACCCGAGA ACCCGGTATC CCGTGTACGG TCTCTCCGT TGCTGAGACC TCTTTGGTAC TCCCACGGT AGAAGCGTTC ACCGACGAGG TCACTACTCG

1501 CAACTTCCCA GAATCTGGC AACAACTACT CTGATGAGCC CTGCATAGA CAGCAGTACC AGATCATCC CCAGATCAAT GGCAACTACG CCCGCTGCT
GTGAAGGT CTAGACCCG TTGTTGATGA GACTACTCG GAGTATCT GTCTCATGG TCTAGTAGCG GGTCTAGTTA CCGTTGATGC GGGCGGACGA

FIG._6B

SEQ ID NO:7

1601 GGACACAGTT CCTCTGGATT ATGAGTTTCT GGCACACTGAG GGCAAAAGTG TCTGTTAAAA ATGCCCCATT AGCCAGGAT CTGCTGACAT AATTGCCTAG
CCTGTGTCAA GGAGACCTAA TACTCAAGA CCGTGACTC CCGTTTTCAC AGACAATTTT TACGGGGTAA TCCGGTCCTA GACGACTGTA TTAACGGATC

1701 TCAGTCCCTG CCTTCTGCAT GGCCTTCTTC CCTGCTACCT CTCTTCCTGG ATAGCCCCAA GTGTCCGCT ACCAACACTG GAGCCGCTGG GAGTCACTGG
AGTCAGGAAC GGAAGACCTA CCGGAAGAAG GGACGATGA GAGAAGGACC TATCGGGTTT CACAGCGGA TGGTTCTGAC CTCGGCGACC CTCAGTGACC

1801 CTTTGCCCTG GAATTGCGA GATGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GCCCTTCTAG TATCTCTGCC GGGGGCTTCT GGTACTCCTC
GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCATTCCGT CGACGACCTA AACCGAGACC CGGAAGATC ATAGAGACGG CCCCCGAAGA CCATGAGGAG

1901 TCTAAATACC AGAGGGAAGA TGCCCATAGC ACTAGGACTT GGTCACTATG CCTACAGACA CTATTCNACT TTGGCATCTT GCCACCAGAA GACCCGAGGG
AGATTTATGG TCTCCCTTCT ACGGTATCG TGATCTGMA CCAGTAGTAC GGATGCTGT GATAAGTTGA AACCGTAGAA CCGTGGTCTT CTGGGCTCCC

2001 AGGCTCAGCT CTGCCAGCTC AGAGGACCAG CTATATCCAG GATCATTTCT CTTTCTTTCAG GCCCAGACAG CTTTAAATTG AAATTGTTAT TTCACAGCCC
TCCGAGTCCA GACGGTCGAG TCTCCTGTC GATATAGGTC CTAGTAAAGA GAAAGMAGTC CCGTCTCTC GMAAATTAAC TTTAACAAATA AAGTGTCCGG

2101 AGGGTTCACT TCTGCTCCTC CACTATAAGT CTAAATGTTCT GACTCTCTCC TGGTCTCMA TAAATATCTA ATCATAACAG C
TCCCAAGTCA AGACGAGGAG GTGATATTCA GATTACAGA CTGACAGAGG ACCACGAGTT ATTTATAGAT TAGTATTGTC G

FIG..6C

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCT
CAGAGCAGCCGGCTGCCGCCCGGGAAGATGGCGAGCAGGAGCCGCCACCGCCTCCTCCT
GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGC
CCCAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA
AACCCCAAGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCTGGAGTGTCTC
CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA
TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT
TAGTGCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT
AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGT
AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGA
TGGCATCCGTTTGTCTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAC
AATGAATACAAAACTGGAAGTCTGCAATTTAATACTGTTTCCAACTGGACACTGGAGA
ATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT
TTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC
CTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGTGCAGTG
GCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGCGGGCGGATCACGAGGTCAGGA
GTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATACAAAATTAG
CTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGCTTGGGAGACAGGAGAATCACTTGA
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGGTAA
CAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATAAATACTGGTTTTTACC
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIG._7

SEQ ID NO:9

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQOTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALW
KAAAGGSRGQEF

FIG._11

SEQ ID NO:5

1 GCAGGCAAG TACCAGGGCC GCCTGCATGT GACCCACMAG GTTCCAGGAG ATGTATCCCT CCAATTGACC ACCCTGGAGA TGCATGACCG GAGCCACTAC
 CGTCCGTTTC ATGCTCCCG CGGACGTACA CTCGGTGTTT CMAAGTCCTC TACATAGGGA GGTAACTCG TGGGACCTCT ACCTACTGGC CTCGGTGATG
 ^42257.f1 SEQ ID NO:18 ^42257.p1 SEQ ID NO:22

101 ACGTGTGAAG TCACCTGGCA GACTCCTCAT GGCACCAAG TCGTGAGAGA TAAGATTACT GAGCTCCGTG TCCAGAACT CTCTGTCTCC AAGCCACAG
TGCACACTTC AGTGGACCGT CTGAGGACTA CCGTGGTTC ACCACTCTCT ATTCTAATGA CTCGAGGCAC AGGTCTTTGA GACACAGAGG TTCGGGTGTC

201 TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT AGCTTCAAT GCCAGGGTTC GGGGTCTCTCC TCCCATCAGT TATATTGCT
 ACTGTTGACC GTCGCCAATA CCGAAGTGCC ACGGGGTCCC TTACTCCTAA TCGGAAGTTA CCGTCCCAAG CCCCAGAGG AGGTAGTCA ATATAAACCA

301 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAGTAG CAACCTAAG TACCTTACTC TTCMAGCCTG CCGTGATAGC CGACTCAGGC TCCTATTCT
 TATTGCTGT CTGATTATTG GTCCCTTGG TACTTTCATC GTTGGGATTC ATGGAATGAG AAGTTCGGAC GCCACTATCG GCTGAGTCCG AGGATAAAGA

401 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCAGAGCGA CATTGTGAAG TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC
CGTGACGGTT CCCGGTCCAA CCGAGACTCG TCGTGTGCTT ^42257.f1 SEQ ID NO:20 ^42257.f2 SEQ ID NO:19

501 TACAACCATG ACATACCCCT TGAAGCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CACTGCTGGG
 ATGTTGGTAC TGTATGGGA ACTTTCGTTG TAGATGTCAC TTGCTCAGGA CCTTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACGACCC

601 CCAGGAAGA GCCTGCCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTG CTGTATGGTG GTTTTACC TGGCCTATAT CATGCTCTCT CGGAAGACAT
 GGTCTTTCT CGGACGGACA GAAACGGTAG TAGGACTAGT AGAGGACAC GACATACCAC CAAAATGGT ACCGATATA GTACAGACA GCCTTCTGTA

701 CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGACATGC CAGAGAGGCC AAGCACTCTG GAGAACCAT GAGGGTGCC ATCTTCGCA GTGGCTGCTC
 GGGTGTCTT CGTACAGATG CTTCGTGGT CCCGTCTACG GTCTCTCCG TTGCTGAGAC CTCTTTGGTA CTCCCACCG TAGAAGCGTT CACCGACGAG

FIG._9A

SEQ ID NO:5

801 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCACAACATA CTCTGATGAG CCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA
GTCACTACTC GGTGGAAGG TCTTAGACCC CGTTGTTGAT GAGACTACTC GGGACGTATC CTCTCCTCAT GGTCTAGTAG CCGGTCTAGT TACCCTTGAT
901 CGCCCGCCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGCTCTTTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC
CGGGGGGAC GACCTGTGTC AAGGAGACCT AATACTCAAA GACCGGTGAC TCCCGTTTTC ACAGACAATT TTTACGGGGT ATCCGGTCC TAGACGACTG
1001 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC CTCTCTTCTT GATAGCCCCA AAGTGTCCGC CTACCAACAC TGGAGCGGCT
TATTAACCGA TCAGTCAGGA ACGBAAGACG TACCGGAAGA AGGGACGATG GAGAGAAGGA CCTATCGGGT TTCACAGGCG GATGGTTGTG ACCTCGGCCA
1101 GGGAGTCACT GGCTTTGCCC TGGAAATTGC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT
CCCTCAGTGA CCGAAACGGG ACCTTAAACG GTCTACGTAG AGTTCATTGG GTCCGACGACC TAAACCGAGA CCGGGGAAGA TCATAGAGAC GGGCCCCGAA
^42257.r2 SEQ ID NO:21

1201 CTGCTACTCC TCTCTAAATA CCAGAGGGAA GATGCCCATTA GCACTAGGAC TTGGTCAATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG
GACCATGAGG AGAGATTTAT GGTCTCCCTT CTACGGGTAT CGTGATCCTG AACCATGATG ACGGATGTCT GTGATAAGTT GAAACCGTAG AACGGTGGTC
1301 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTCT
TTCTGGGCTC CCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCCTACTAA AGAGAAAGAA GTCCGGGTCT GTCGAAAATT AACTTTAACA
1401 TATTTACAG GCCAGGGGTC AGTTCTGCTC CTCCTACTATA AGTCTAATCT TCTGACTCTC TCCTGTGTCT CAATAAATAT CTAATCATAA CAGCAAAAAA
ATAAAGTCTC CGCTCCCAAG TCAAGACGAG CAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCACCA GTTATTATTA GATTAGTATT GTCGTTTTTT

1501 AAA

TTT

FIG._9B

PCT 30

A33 HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%). POSITIVES = 131/268 (48%). AT 121, 17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPR-- --VEW-KEDQGDTRLVC--YNN

SEQ ID NO:23

DNA40628 283 K--ITAS-YEDRVTF-----PTGITFKSVTREDTGTTCMVS--EEGNSYGEVVKVK

A33 human 77 KNYIHGELYKNRVVISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT--KSRVR

DNAA0628 427 L LVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPSEYTWFKDGVMPNTNPKSTRAFSN

A33 human 135 LLVLVPPSKPECGIEGETIIGNNIQLTCQSKESGPTPQYSWKRYNILLNQEQP-----

DNA40628 607 SSVLNPPTGELV-FDPLSASDTGEYSCEARNGYGTPTMTSNAVRMEAVERNVGV--IVA

122 human 187 ---1.AOPASGOPVSLKNISTDTSGYICTSSNEEGTOFCNITVAVRSPSMNVALYVGIAV

DNAA40628 775 AVLVTLILLGILVFGIWFAYSRGHFDRT--KKGTSKKVIYSQP

[illegible]

FIG. 10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19

SEQ ID NO:25

SEQ ID NO:26

מבוא

A33 - Immunology

DN47020

A33 human

DNA40628

A33 human

FIG. 10B

FIG. 10B

SEQ ID NO: 6 A33_hum 1 M V G K M W P V L W T L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L
SEQ ID NO: 1 40628 1 M G T K A Q V E R K L L C L F I L A I L L C S . . L A L G S V T V H S S E P E V R I P E N N P V K L

A33_hum 42 P C T Y H T S T S R E G L I O W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I
40628 49 S C A Y S G F S S P R . . . V E W . K F D Q G D T T R L V C . . Y N N K . . I T A S . Y E D R V T F

A33_hum 92 S N H A E O S D A S I T I D Q L T M A D N G T Y E C S V S L M S D L E G N T K S R V R L L V L V P P
40628 90 L P T G I T F K S V T R E D T G T Y T C H V S E E G G . N S Y G E V K V K L I I V L V P P

A33_hum 142 S K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q P
40628 133 S K P T V N I P S S A T I G N R A V L T C S E Q D G S P S E Y T W F K D G I V M P T N P K S T R A

A33_hum 187 L A Q P A S G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T Q F C N I T V A V R S
40628 183 F S N S S Y V L N P T T G E . L V F D P L S A S D T G E Y S C E A R N G Y G T P M T S H A V R M E A

A33_hum 231 P S M N V A L Y V G I A V G V V A A L I I G I I I Y C C . C C R G K D D N T E D K E D A R P N R E
40628 232 V E R N V G V . . . I V A A V L V T L I L L G I L V F G I W F A Y S R G H F D R T K K G T S S K K V

A33_hum 280 A Y E E P P E Q L R E L S R E R E E E D D Y R Q E E O R S T G R E S P D H L D O
40628 279 I Y S Q P S A R S E G E F K Q T S S F L V

FIG..12

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SEQID NO: 6  A33_hum  1  M V G K M W P V L W T L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T Y H T S T S
SEQID NO: 2  45416  1  - M G I L L G L L L G H L T V D T Y G R P I L E V P E S V T G P W K G - D V N L P C T Y D P L O G

A33_hum      51  S R E G L I Q W D K L L L T H T E R V V I I W - P F S N K N Y I I H G E L Y K N R V S I S N N A E Q S D
45416        49  Y T Q V L V K W - - L V Q R G S D P V T I I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V - P G D

A33_hum     100  A S I T I D Q L T M A D N G T Y E C S V S - L M S D L E G N T K S R V - - - - - R L L V L V P P S
45416        96  V S L Q L S T L E M D O R S H Y T C E V T W O T P D G N Q V V R D K I T E L R V Q K L S V S K P T V

A33_hum     143  K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A Q P A S
45416       146  T T G S G Y G F T V P Q G M R I S L Q C Q A R - G S P I S Y I W - - Y K Q Q T N N Q E P I K V A T

A33_hum     193  G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T - Q F C N I - T V A V R S P S M N V A L Y V G
45416       193  L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I I V K F V V K D S S K L L K T K T E

A33_hum     241  I A V G V V A A L I I I G I I I Y C C C C R G K D D N T E D K E D A R P N R E A Y E E P P E Q L R E
45416       243  A P T T M T Y P L K A T S T V K S W D W T T D M D G Y L G E T S A G P G K S L P V F A I I L I S

A33_hum     291  L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
45416       293  L C C H V V F T M A Y I M L C R K T S Q Q E H V Y E A A R

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FIG.-13

1 . . HVGKMWPLWTLLCAVRYTVD . . . A I S V E T P O D V L R A S Q G K S V T L P C
1 MARRSRHRLLLLLRYLVVALGYHKAYGFSAPKDOQVVTATAVEYQEA I L A C

1 MARRSRHRLLLRLLRYLVVALGYHKA YGFSAPKDDQQV VTYA V EYQEA I LAC

44 TYHTSTSSREGLIQWDKLLTHTERVVIPWFSNKXNYIHGELYXNRVSI
51 ..KTPKKTVSSRLEWKKL...GRSVSFVYYQQT.LQGD.FKNR.....

51 .. K I P X K T V S S R L E W K K L G R S V S F V Y Y Q O T . L O G D . F K N R

94 NAEQSDASITIIDOLTHADNGTYECSSVLSMSDLEGN.TXSRVRLVLVPPPS
87 .AEMIDFNIRIKNVTRSDAGKYRCEVSAPEQGNLEEDTVTLVLAFA

87 - A E M I O F N I R I K N V T R S D A G K Y R C E V S A P S E Q G N L E E D I V I L E V L V A P A

143. K P E C G I E G E T I I G N I Q L T C O S K E G S P T P Q Y S W K R Y N I L N Q E O P L A Q P A S

136 V P S C E V P S S A L S G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L E N P R L G S Q S

136 V P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G J R L L E N P R L G S Q S

193 G Q P V S L K N I S T D T S G Y I C T S S N E E G T O F C N I T V A V . . . R S P S M N V A L Y V
186 T N S S Y T M N T K T T G T L O F N T . V S K L D T G E Y S C E A R N S V G Y R R C P G K R M Q V D D

186 T N S S Y T M I N T X T G T L Q F N T . V S K L D T G E Y S C E A R N S V G Y R R C P G K R M O V D D

240	G	I	A	V	G	V	V	A	L	I	I	G	I	I	Y	C	C	R	G	K	D	D	N	T	E	K	E	D	A	R	P	N	R	E	A	Y	E	E	P	E						
235	L	N	I	S	G	I	I	A	V	V	V	A	L	V	I	S	V	C	G	L	G	V	C	Y	A	O	R	K	G	Y	F	S	K	E	T	S	F	O	K	S	N	S	S	K	A	T

235 L N I S G I I A A V V V V A L V I I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S K A T T

287 QL R E L S A . E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
285 M S E N V Q W L T P V I P A L W K A A G G S R G Q E F

285 M S E N V Q W L T P V I P A L W K A A G G S R G Q E F F

SEQ ID NO: 10 jam 1 MGT E G K A G R K L L F L F T - S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L T C
 SEQ ID NO: 1 40628 1 MGT K A Q V E R K L L C L F I L A I L L C S L A L G S V T V H S S E P E V R I P E N N P V K L S C

jam 50 T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S S V T
 40628 51 A Y S G F S S P R V E W K F D Q G D T T R L V C Y N N K I T A S Y E D R V T F L P T G I T F K S V T

jam 100 R K D N G E Y T C M V S E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I G N R A V
 40628 101 R E D T G T Y T C M V S E E G G N S Y G E V K V K L I V L V P P S K P T V N I P S S A T I G N R A V

jam 150 L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S G D L I F
 40628 151 L T C S E Q D G S P P S E Y T W F K D G I . V M P T N P K S T R A F S N S S Y V L N P T T G E L V F

jam 200 D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L N V G G I V A A V L V T L I L
 40628 200 D P L S A S D T G E Y S C E A R N G Y G T P W T S N A V R M E A V E R N V G V I V A A V L V T L I L

jam 250 L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R S E G E F K Q T S S F L
 40628 250 L G I L V F G I W F A Y S R G H F D R T K K G T . S S K K V I Y S Q P S A R S E G E F K Q T S S F L

jam 300 V
 40628 299 V

FIG.-15

20 / 24

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L T
 SEQ ID NO: 2 45416 1 M G I L L G L L L G H L T V D T Y G R P I L E V P E S V T G P W K G D V N L P

49 C T Y S . . . G F S S P R V E W K F V Q G S T T A L V . . . C Y N S Q I T A P Y A D R V T F S .
 45416 41 C T Y D P L Q G Y T Q V L V K W L V Q R G S O P V T I F L R D S S G D H I Q Q A K Y Q Q R L H V S H

90 S S G I T F S S V T R K D N G E Y T C M V . . . S E E G G Q N Y G E V S I H L T V L V P P
 45416 91 K V P G D V S L Q L S T L E M D O R S H Y T C E V T W O T P D G N Q V V R D K I T E L R V Q K L S V

132 S K P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A
 45416 141 S K P T V T T G S G Y G F T V P Q G M R I S L Q C Q A R G S P P I S Y I W Y K Q O T N . . N Q E P

178 K K T R A F M N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A
 45416 188 I K V A T L S T L L F K P A V I A D S G S Y F C T A K G O V G S E Q H S D I V

228 H . . . M D A V E L N V G G I V A A V L V T L I L G L L I F G . . . V W F A Y S R G Y F E T T K K
 45416 227 K F V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W D W T T D M D G Y L G E T S A

jam 272 G T A P G K K V I Y S O P S T R S E G E F K Q T S S F L V
 45416 277 G P G K S L P V F A I I L I S L C C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R

FIG. 16

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SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q S D V Q V . . . P E N E S I K L
SEQ ID NO: 29 35638 1 . . W A R R S R H R L L L L R Y L V V A L G Y H K A Y G F S A P K Q Q V T A V E Y O E A I L

jam 48 T C . T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S
35638 49 A C K T P K X T V S S R L E W K K L . G R S V S F V Y Y Q Q T L Q G D F K N R A E M I D F N I R I K

jam 97 S V T R K D N G E Y T C M V S . . E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I
35638 98 N V T R S D A G K Y R C E V S A P S E Q G Q N L E E D T V T L E V L V A P A V P S C E V P S S A L S

jam 145 G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S
35638 148 G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L . E N P R L G S Q S T N S S Y T M N T K T

jam 195 G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A H R S E A A H M D A V E L N V G I V A A V L
35638 197 G T L Q F N T V S K L D T G E Y S C E A R N S V G . Y R R C P G K R W Q V D D L N I S G I I A A V V

jam 245 V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R S E G E F K Q
35638 246 V V A L V I S V C G L G V C Y A Q R K G Y F . . . S K E T S F O K S N S S S K A T T M S E N V Q W L

jam 295 T S S F L V
35638 293 T P V I P A L W K A A A G G S R G Q E F

FIG._17

+

SEQ ID NO: 6 A33_hum 1 M V G K M W P V L W T . L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T
 SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q S D V O V P E N E S I K L T C T

A33_hum 45 Y H T S T S S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I I H G E L Y K N R V S I S N N
 jam 51 Y S G F S S P R . . . V E W . K F V O G S T T A L V C . . Y N S Q . . I T A P . Y A D R V T F S S .

A33_hum 95 A E Q S D A S I T I D Q L T M A D N G T Y E C S V S L M S D L E G N T K S R V R L L V L V P P S K P
 jam 91 S G I T F S S V T R K D N G E Y T C M V S E E G G . Q N Y G E V S I H L T V L V P P S K P

A33_hum 145 E C G I E G E T I I G N N I Q L T C Q S K E G S P T P O Y S W K R Y N I L N Q E Q P L A Q P A S G Q
 jam 135 T I S V P S S V T I G N R A V L T C S E H D G S P S E Y S W F K D G I S M L T A D A K K T R A F M

A33_hum 195 P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N I T V A V R S P S M N . . . V A L
 jam 185 N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L

A33_hum 238 Y V . G I A V G V V A A L I I G I I I Y C . . . C C C R G K D D N T E D K E D A R P N R E A Y E E
 jam 235 N V G G I V A A V L V T L I L L G L L I F G V W F A Y S R G Y F E . T T K K G T A P G K K V I Y S Q

A33_hum 284 P P E O L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
 jam 284 P S T R S E G E F K Q T S S F L V

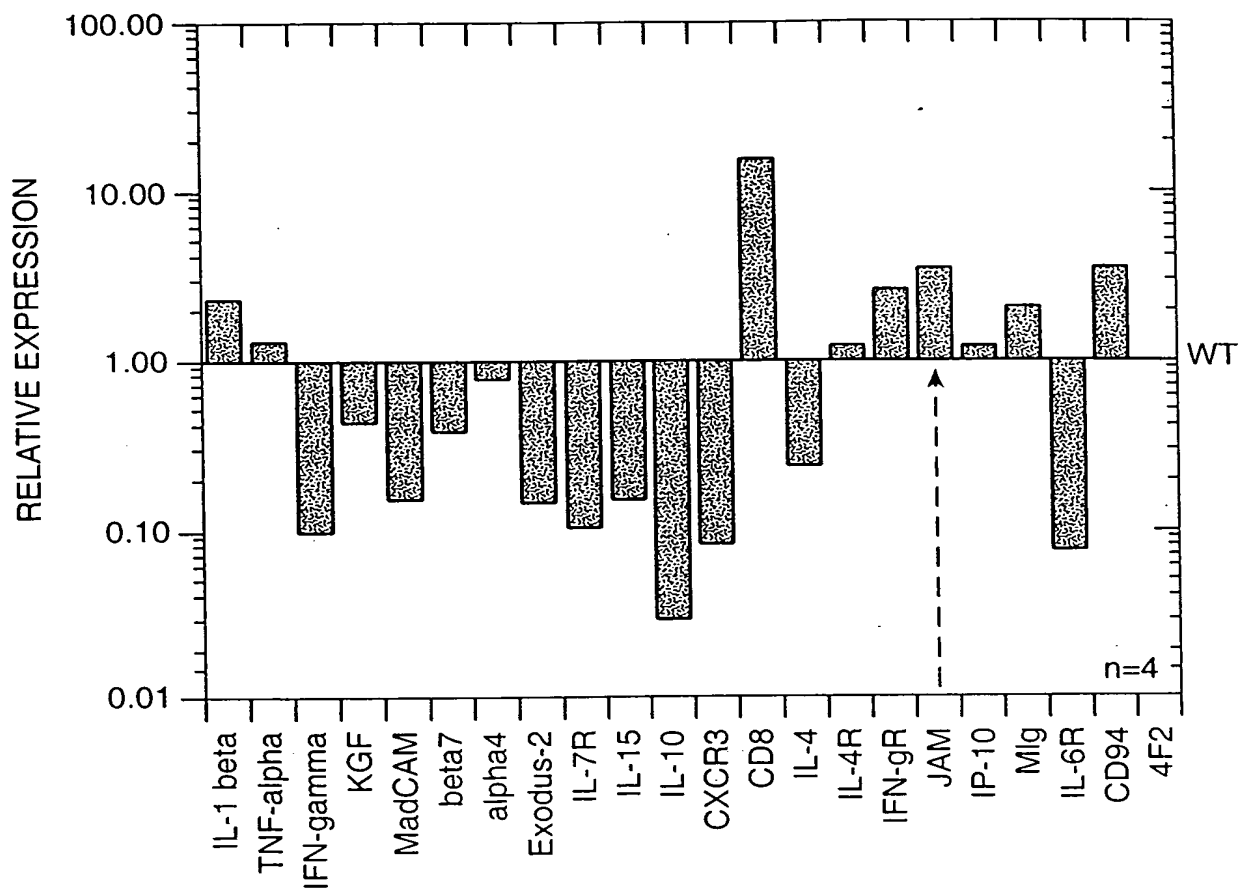
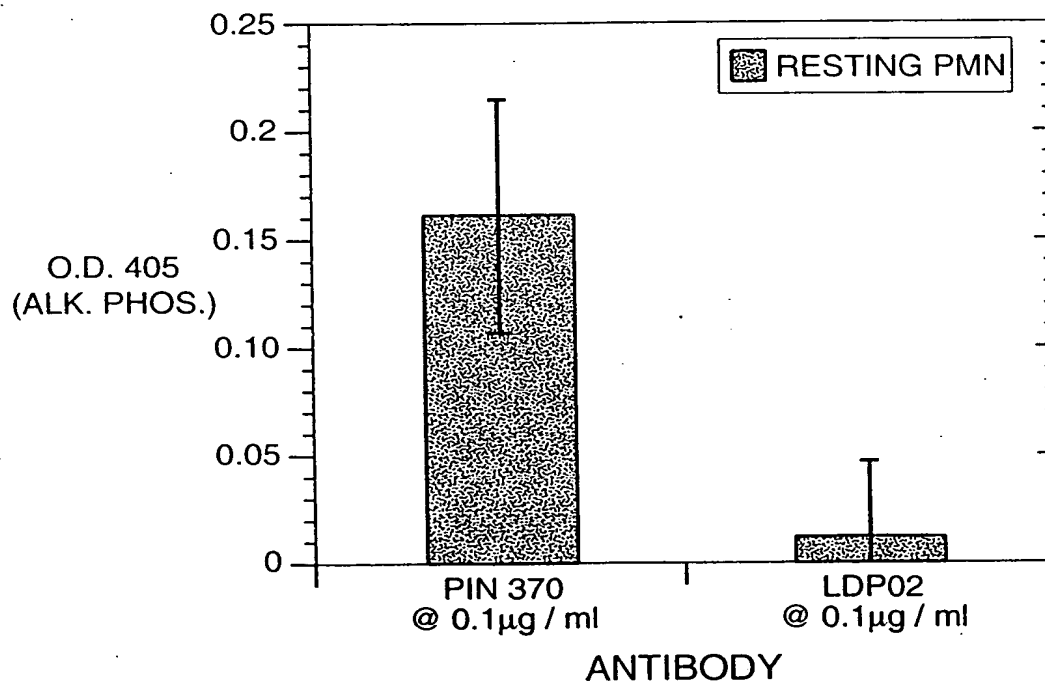
FIG.-18

23 / 24

<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++		
PUTAMEN	+	OVARY	+++	APPENDIX	+
SUSTANTIA NIGRA	+	PANCREAS	++	LUNG	++++
TEMPORAL LOBE	+	PITUITARY GLAND	++	TRACHEA	++++
THALAMUS	+	ADRENAL GLAND	++	PLACENTA	++++
NUCLEUS ACCUMBEUS	+	THYROID GLAND	++		
SPINAL CORD	-	SALIVARY GLAND	+++	FETAL BRAIN	+
		MAMMARY GLAND	++	FETAL HEART	+
				FETAL KIDNEY	++
				FETAL LIVER	+++
				FETAL SPLEEN	+
				FETAL LUNG	++++

FIG._19

24 / 24

**FIG. 20****FIG. 21**